Andrew Almond

List of Publications by Year
in descending order

57 papers	2,556 citations	136950 32 h-index	197818 49 g-index
58 all docs	58 docs citations	58 times ranked	2433 citing authors

#	Article	IF	Citations
1	Deconvolution of conformational exchange from Raman spectra of aqueous RNA nucleosides. Communications Chemistry, 2020, 3, .	4.5	7
2	Multiscale modeling of glycosaminoglycan structure and dynamics: current methods and challenges. Current Opinion in Structural Biology, 2018, 50, 58-64.	5.7	51
3	Synthesis and characterization of heparosan-granulocyte-colony stimulating factor conjugates: a natural sugar-based drug delivery system to treat neutropenia. Glycobiology, 2017, 27, 1052-1061.	2.5	20
4	Heparosan-coated liposomes for drug delivery. Glycobiology, 2017, 27, 1062-1074.	2.5	31
5	Chemical polyglycosylation and nanolitre detection enables single-molecule recapitulation of bacterial sugar export. Nature Chemistry, 2016, 8, 461-469.	13.6	26
6	Proteoglycans and Their Heterogeneous Glycosaminoglycans at the Atomic Scale. Biomacromolecules, 2015, 16, 951-961.	5.4	35
7	A Refined Model for the TSG-6 Link Module in Complex with Hyaluronan. Journal of Biological Chemistry, 2014, 289, 5619-5634.	3.4	46
8	Catechol-hydrazone conjugates for the rapid functionalization of magnetite nanoparticles with cell targeting groups. Materials Research Society Symposia Proceedings, 2014, 1688, 1.	0.1	2
9	Microsecond kinetics in model single- and double-stranded amylose polymers. Physical Chemistry Chemical Physics, 2014, 16, 8119-8126.	2.8	21
10	Shaping up for structural glycomics: a predictive protocol for oligosaccharide conformational analysis applied to N-linked glycans. Carbohydrate Research, 2014, 383, 34-42.	2.3	22
11	Does Microsecond Sugar Ring Flexing Encode 3D-Shape and Bioactivity in the Heparanome?. Biomacromolecules, 2013, 14, 1149-1159.	5.4	56
12	Quantification of free ligand conformational preferences by NMR and their relationship to the bioactive conformation. Bioorganic and Medicinal Chemistry, 2013, 21, 4976-4987.	3.0	45
13	Assigning kinetic 3D-signatures to glycocodes. Physical Chemistry Chemical Physics, 2012, 14, 5843.	2.8	19
14	Dependence of Pyranose Ring Puckering on Anomeric Configuration: Methyl Idopyranosides. Journal of Physical Chemistry B, 2012, 116, 6380-6386.	2.6	35
15	Pd(II)-Mediated Assembly of Porphyrin Channels in Bilayer Membranesâ€. Langmuir, 2011, 27, 1448-1456.	3.5	33
16	Is N-acetyl-d-glucosamine a rigid 4C1 chair?. Glycobiology, 2011, 21, 1651-1662.	2.5	53
17	Less is more when simulating unsulfated glycosaminoglycan 3Dâ€structure: Comparison of GLYCAM06/TIP3P, PM3â€CARB1/TIP3P, and SCCâ€DFTBâ€D/TIP3P predictions with experiment. Journal of Computational Chemistry, 2010, 31, 2932-2947.	3.3	28
18	A 3D-structural model of unsulfated chondroitin from high-field NMR: 4-sulfation has little effect on backbone conformation. Carbohydrate Research, 2010, 345, 291-302.	2.3	51

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19	A New Route to Carbohydrate Secondary and Tertiary Structure Using Raman Spectroscopy and Raman Optical Activity. Journal of the American Chemical Society, 2010, 132, 10654-10655.	13.7	45
20	Free Energy Landscapes of Iduronic Acid and Related Monosaccharides. Journal of the American Chemical Society, 2010, 132, 13132-13134.	13.7	86
21	Investigating the Molecular Basis for the Virulence of <i>Escherichia coli</i> K5 by Nuclear Magnetic Resonance Analysis of the Capsule Polysaccharide. Journal of Molecular Microbiology and Biotechnology, 2009, 17, 71-82.	1.0	20
22	Comparative pharmacology and computational modelling yield insights into allosteric modulation of human Î±7 nicotinic acetylcholine receptors. Biochemical Pharmacology, 2009, 78, 836-843.	4.4	40
23	The Conformational Properties of the Glc3Man Unit Suggest Conformational Biasing within the Chaperone-assisted Glycoprotein Folding Pathway. Journal of Molecular Biology, 2009, 387, 335-347.	4.2	22
24	The structural plasticity of heparan sulfate NA-domains and hence their role in mediating multivalent interactions is confirmed by high-accuracy 15N-NMR relaxation studies. Glycoconjugate Journal, 2008, 25, 401-414.	2.7	40
25	Determining the Molecular Basis for the pH-dependent Interaction between the Link Module of Human TSG-6 and Hyaluronan. Journal of Biological Chemistry, 2007, 282, 12976-12988.	3.4	31
26	N-Acetylated amino sugars: the dependence of NMR 3J(HNH2)-couplings on conformation, dynamics and solvent. Organic and Biomolecular Chemistry, 2007, 5, 2243.	2.8	49
27	Using Molecular Dynamics Simulations To Provide New Insights into Protein Structure on the Nanosecond Timescale:â€‰ Comparison with Experimental Data and Biological Inferences for the Hyaluronan-Binding Link Module of TSG-6. Journal of Chemical Theory and Computation, 2007, 3, 1-16.	5.3	16
28	Temperature dependencies of amide1H- and15N-chemical shifts in hyaluronan oligosaccharides. Magnetic Resonance in Chemistry, 2007, 45, 430-433.	1.9	20
29	Fourier transform mass spectrometry to monitor hyaluronan-protein interactions: use of hydrogen/deuterium amide exchange. Rapid Communications in Mass Spectrometry, 2007, 21, 121-131.	1.5	14
30	Hyaluronan. Cellular and Molecular Life Sciences, 2007, 64, 1591-1596.	5.4	173
31	The importance of including local correlation times in the calculation of inter-proton distances from NMR measurements: ignoring local correlation times leads to significant errors in the conformational analysis of the GlcÎ±1â€“2GlcÎ± linkage by NMR spectroscopy. Organic and Biomolecular Chemistry, 2006, 4, 2241-2246.	2.8	9
32	Experimental evidence for all-or-none cooperative interactions between the G1-domain of versican and multivalent hyaluronan oligosaccharides. Matrix Biology, 2006, 25, 14-19.	3.6	13
33	Hyaluronan: The Local Solution Conformation Determined by NMR and Computer Modeling is Close to a Contracted Left-handed 4-Fold Helix. Journal of Molecular Biology, 2006, 358, 1256-1269.	4.2	102
34	Biomolecular Dynamics: Testing Microscopic Predictions against Macroscopic Experiments. ACS Symposium Series, 2006, , 156-169.	0.5	3
35	Hyaluronan: the absence of amideâ€“carboxylate hydrogen bonds and the chain conformation in aqueous solution are incompatible with stable secondary and tertiary structure models. Biochemical Journal, 2006, 396, 487-498.	3.7	58
36	NMR spectra of oligosaccharides at ultra-high field (900MHz) have better resolution than expected due to favourable molecular tumbling. Carbohydrate Research, 2006, 341, 1985-1991.	2.3	17

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37	Enzymatic and chemical methods for the generation of pure hyaluronan oligosaccharides with both odd and even numbers of monosaccharide units. Analytical Biochemistry, 2006, 353, 236-247.	2.4	26
38	Defined megadalton hyaluronan polymer standards. Analytical Biochemistry, 2006, 355, 183-188.	2.4	22
39	Complete assignment of hyaluronan oligosaccharides up to hexasaccharides. Carbohydrate Research, 2006, 341, 2803-2815.	2.3	38
40	Exploiting the carboxylate chemical shift to resolve degenerate resonances in spectra of13C-labelled glycosaminoglycans. Magnetic Resonance in Chemistry, 2005, 43, 805-815.	1.9	11
41	Towards understanding the interaction between oligosaccharides and water molecules. Carbohydrate Research, 2005, 340, 907-920.	2.3	90
42	Preparation and application of biologically active fluorescent hyaluronan oligosaccharides. Glycobiology, 2005, 15, 303-312.	2.5	37
43	Expression and Purification of Functionally Active Hyaluronan-binding Domains from Human Cartilage Link Protein, Aggrecan and Versican. Journal of Biological Chemistry, 2005, 280, 5435-5448.	3.4	82
44	Towards a Structure for a TSG-6Â·Hyaluronan Complex by Modeling and NMR Spectroscopy. Journal of Biological Chemistry, 2005, 280, 18189-18201.	3.4	69
45	Dynamics of Hyaluronan Oligosaccharides Revealed by 15N Relaxation. Journal of the American Chemical Society, 2005, 127, 1086-1087.	13.7	32
46	Use of 15N-NMR to resolve molecular details in isotopically-enriched carbohydrates: sequence-specific observations in hyaluronan oligomers up to decasaccharides. Glycobiology, 2004, 14, 999-1009.	2.5	56
47	Oligosaccharides Implicated in Recognition Are Predicted to Have Relatively Ordered Structures. Biochemistry, 2004, 43, 5853-5863.	2.5	44
48	Predicting the molecular shape of polysaccharides from dynamic interactions with water. Glycobiology, 2003, 13, 255-264.	2.5	78
49	The Link Module from Ovulation- and Inflammation-associated Protein TSG-6 Changes Conformation on Hyaluronan Binding. Journal of Biological Chemistry, 2003, 278, 49261-49270.	3.4	81
50	Physical Interpretation of Residual Dipolar Couplings in Neutral Aligned Media. Journal of the American Chemical Society, 2002, 124, 9986-9987.	13.7	78
51	Comparison of Aqueous Molecular Dynamics with NMR Relaxation and Residual Dipolar Couplings Favors Internal Motion in a Mannose Oligosaccharide. Journal of the American Chemical Society, 2001, 123, 4792-4802.	13.7	54
52	Quantitative conformational analysis of the core region of N-glycans using residual dipolar couplings, aqueous molecular dynamics, and steric alignment. , 2001, 20, 351-363.		31
53	Glycosaminoglycan conformation: do aqueous molecular dynamics simulations agree with x-ray fiber diffraction?. Glycobiology, 2000, 10, 329-338.	2.5	58
54	Deducing polymeric structure from aqueous molecular dynamics simulations of oligosaccharides: predictions from simulations of hyaluronan tetrasaccharides compared with hydrodynamic and X-ray fibre diffraction data 1 1Edited by R. Huber. Journal of Molecular Biology, 1998, 284, 1425-1437.	4.2	72

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55	Dynamic exchange between stabilized conformations predicted for hyaluronan tetrasaccharides: Comparison of molecular dynamics simulations with available NMR data. Glycobiology, 1998, 8, 973-980.	2.5	63
56	Molecular dynamics simulations of the two disaccharides of hyaluronan in aqueous solution. Glycobiology, 1997, 7, 597-604.	2.5	57
57	Structural characterisation of two forms of procyclic acidic repetitive protein expressed by procyclic forms of Trypanosoma brucei. Journal of Molecular Biology, 1997, 269, 529-547.	4.2	138